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1

SEQUENCE LISTING

<110> ZIMMET, PAUL Z.  
COLLIER, GREGORY

<120> A NOVEL GENE AND USES THEREFOR

<130> 22975-20007.00

<140> 09/331,930

<141> 1999-06-30

<150> PCT/AU98/00902

<151> 1998-10-30

<150> AU PP0117/97

<151> 1997-10-31

<150> AU PP0323/97

<151> 1997-11-11

<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 342

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: DNA sequence for  
beacon from unknown organism

<220>

<221> CDS

<222> (29)..(247)

<400> 1

gttccaggag attacagctc cagccaca atg att gag gtg gtt tgc aac gac 52  
Met Ile Glu Val Val Cys Asn Asp  
1 5

cgt cta gga aag aaa gtc cgc gtt aag tgc aac acc gat gac acc atc 100  
Arg Leu Gly Lys Lys Val Arg Val Lys Cys Asn Thr Asp Asp Thr Ile  
10 15 20

ggg gac ttg aag aaa ctg ata gcg gcc caa act ggc act cgt tgg aat 148  
Gly Asp Leu Lys Lys Leu Ile Ala Ala Gln Thr Gly Thr Arg Trp Asn  
25 30 35 40

aag atc gtt ctt aaa aag tgg tac acg att ttt aag gac cat gta tct 196  
Lys Ile Val Leu Lys Lys Trp Tyr Thr Ile Phe Lys Asp His Val Ser  
45 50 55

ctg gga gat tat gaa atc cac gat ggg atg aac ctg gag ctt tat tac 244  
Leu Gly Asp Tyr Glu Ile His Asp Gly Met Asn Leu Glu Leu Tyr Tyr  
60 65 70



57

A

cag tagaggggaa ttctccacc ttgcccaacc ttgctttcct ctcccatggc 297  
Gln

tcatttaaca ctgttgtaga tgctcatttt tttgttaagt gtact 342

<210> 2

<211> 73

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Amino acid  
sequence for beacon from unknown organism

<400> 2

Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Arg Val  
1 5 10 15

Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala  
20 25 30

Ala Gln Thr Gly Thr Arg Trp Asn Lys Ile Val Leu Lys Lys Trp Tyr  
35 40 45

Thr Ile Phe Lys Asp His Val Ser Leu Gly Asp Tyr Glu Ile His Asp  
50 55 60

Gly Met Asn Leu Glu Leu Tyr Tyr Gln  
65 70

<210> 3

<211> 391

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Complimentary  
sequence for SEQ ID NO: 1

<400> 3

atgttcaaca cagcagccat ccaaggtcct ctaatgtcga ggtcggtggt actaactcca 60  
ccaaacgttg ctggcagatc ctttctttca ggcgcaattc acgttgtggc tactgtggta 120  
gcccctgaac ttctttgact atcgccgggt ttgaccgtga gcaaccttat tctagcaaga 180  
atttttcacc atgtgctaaa aattcctggt acatagagac cctctaatac tttaggtgct 240  
accctacttg gacctcgaaa taatggtcat ctccccttaa ggaggtggaa cgggttgga 300  
cgaaaggaga gggtagcgag taaattgtga caacatctac gagtaaaaaa acaattcaca 360  
tgaataaaaa ctttgatgct gcaaaaaaaa a 391

<210> 4

<211> 16

<212> DNA

<213> Artificial Sequence

52

A

<220>  
<223> Description of Artificial Sequence: Primer  
  
<400> 4  
aagctttttt tttttg 16  
  
<210> 5  
<211> 13  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Primer  
  
<400> 5  
aagcttcggg taa 13  
  
<210> 6  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Primer  
  
<400> 6  
agtccgcgtt aagtgaaca 20  
  
<210> 7  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Primer  
  
<400> 7  
ctccaggttc atcccatcgt 20  
  
<210> 8  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Primer  
  
<400> 8  
ggctacagct tcaccaccac 20  
  
<210> 9  
<211> 20  
<212> DNA

53

A

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 9

gcttgctgat ccacatctgc

20

<210> 10

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe

<400> 10

tggtataaaa gctccaggtt catcccatcg

30

<210> 11

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 11

caaactggca ctcgttggaa

20

<210> 12

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 12

gttgggcaag gtggaggaa

19

<210> 13

<211> 102

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(99)

<220>

<221> modified\_base

<222> (44)

<223> a, t, c or g

54

A

<400> 13  
 atg atc gag gtt gtt tgc aac gac cgt ctg ggg aaa aag gtc cnc gtt 48  
 Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Xaa Val  
 1 5 10 15  
 aaa tgc aac acg gat gat acc atc ggg gac ctt aag aag ctg att gca 96  
 Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala  
 20 25 30  
 gcc taa 102  
 Ala

<210> 14  
 <211> 33  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MOD\_RES  
 <222> (15)  
 <223> variable amino acid

<400> 14  
 Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Xaa Val  
 1 5 10 15  
 Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala  
 20 25 30  
 Ala

<210> 15  
 <211> 222  
 <212> DNA  
 <213> Psammomys obesus

<220>  
 <221> CDS  
 <222> (1)..(99)

<400> 15  
 aag atc gtt ctt aaa aag tgg tac acg att ttt aag gac cat gta tct 48  
 Lys Ile Val Leu Lys Lys Trp Tyr Thr Ile Phe Lys Asp His Val Ser  
 1 5 10 15  
 ctg gga gat tat gaa atc cac gat ggg atg aac ctg gag ctt tat tac 96  
 Leu Gly Asp Tyr Glu Ile His Asp Gly Met Asn Leu Glu Leu Tyr Tyr  
 20 25 30  
 cag tagaggggaa ttctccacc ttgcccaacc ttgctttcct ctcccatggc 149  
 Gln  
 tcatttaaca ctgttgtaga tgctcatttt taacaattca catgaataaa aactttgatg 209

55

A

ctgcaaaaaa aaa

222

&lt;210&gt; 16

&lt;211&gt; 33

&lt;212&gt; PRT

&lt;213&gt; Psammomys obesus

&lt;400&gt; 16

Lys	Ile	Val	Leu	Lys	Lys	Trp	Tyr	Thr	Ile	Phe	Lys	Asp	His	Val	Ser
1				5					10					15	

Leu	Gly	Asp	Tyr	Glu	Ile	His	Asp	Gly	Met	Asn	Leu	Glu	Leu	Tyr	Tyr
		20						25					30		

Gln

&lt;210&gt; 17

&lt;211&gt; 222

&lt;212&gt; DNA

&lt;213&gt; Psammomys obesus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (99)

&lt;400&gt; 17

aag	atc	gtt	ctt	aaa	aag	tgg	tac	acg	att	ttt	aag	gac	cat	gta	tct	48
Lys	Ile	Val	Leu	Lys	Lys	Trp	Tyr	Thr	Ile	Phe	Lys	Asp	His	Val	Ser	
1				5					10					15		

ctg	gga	gat	tat	gaa	atc	cac	gat	ggg	atg	aac	ctg	gag	ctt	tat	tac	96
Leu	Gly	Asp	Tyr	Glu	Ile	His	Asp	Gly	Met	Asn	Leu	Glu	Leu	Tyr	Tyr	
		20						25					30			

cag	tagaggggaa	ttcctccacc	ttgcccaacc	ttgctttcct	ctcccatggc	149
Gln						

tcatttaaca	ctgttgtaga	tgctcatttt	taacaattca	catgaataaa	aactttgatg	209
------------	------------	------------	------------	------------	------------	-----

ctgcaaaaaa aaa

222

&lt;210&gt; 18

&lt;211&gt; 33

&lt;212&gt; PRT

&lt;213&gt; Psammomys obesus

&lt;400&gt; 18

Lys	Ile	Val	Leu	Lys	Lys	Trp	Tyr	Thr	Ile	Phe	Lys	Asp	His	Val	Ser
1				5					10					15	

Leu	Gly	Asp	Tyr	Glu	Ile	His	Asp	Gly	Met	Asn	Leu	Glu	Leu	Tyr	Tyr
		20						25					30		

Gln

56

A

<210> 19  
 <211> 73  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: Amino acid  
 sequence for beacon from unknown organism

<400> 19  
 Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Arg Val  
           1                  5                  10                  15  
 Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala  
                   20                  25                  30  
 Ala Gln Thr Gly Thr Arg Trp Asn Lys Ile Val Leu Lys Lys Trp Tyr  
                   35                  40                  45  
 Thr Ile Phe Lys Asp His Val Ser Leu Gly Asp Tyr Glu Ile His Asp  
           50                  55                  60  
 Gly Met Asn Leu Glu Leu Tyr Tyr Gln  
           65                  70

<210> 20  
 <211> 73  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Arg Val  
           1                  5                  10                  15  
 Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala  
                   20                  25                  30  
 Ala Gln Thr Gly Thr Arg Trp Asn Lys Ile Val Leu Lys Lys Trp Tyr  
                   35                  40                  45  
 Thr Ile Phe Lys Asp His Val Ser Leu Gly Asp Tyr Glu Ile His Asp  
           50                  55                  60  
 Gly Met Asn Leu Glu Leu Tyr Tyr Gln  
           65                  70

<210> 21  
 <211> 73  
 <212> PRT  
 <213> Murine sp.

57

A

&lt;400&gt; 21

Met	Ile	Glu	Val	Val	Cys	Asn	Asp	Arg	Leu	Gly	Lys	Lys	Val	Arg	Val
1				5					10					15	

Lys	Cys	Asn	Thr	Asp	Asp	Thr	Ile	Gly	Asp	Leu	Lys	Lys	Leu	Ile	Ala
			20					25					30		

Ala	Gln	Thr	Gly	Thr	Arg	Trp	Asn	Lys	Ile	Val	Leu	Lys	Lys	Trp	Tyr
		35					40					45			

Thr	Ile	Phe	Lys	Asp	His	Val	Ser	Leu	Gly	Asp	Tyr	Glu	Ile	His	Asp
	50					55					60				

Gly	Met	Asn	Leu	Glu	Leu	Tyr	Tyr	Gln
65					70			

&lt;210&gt; 22

&lt;211&gt; 73

&lt;212&gt; PRT

&lt;213&gt; Caenorhabditis elegans

&lt;400&gt; 22

Met	Ile	Glu	Ile	Thr	Val	Asn	Asp	Arg	Leu	Gly	Lys	Lys	Val	Arg	Ile
1				5					10					15	

Lys	Cys	Asn	Pro	Ser	Asp	Thr	Ile	Gly	Asp	Leu	Lys	Lys	Leu	Ile	Ala
			20					25					30		

Ala	Gln	Thr	Gly	Thr	Arg	Trp	Glu	Lys	Ile	Val	Leu	Lys	Lys	Trp	Tyr
		35					40					45			

Thr	Ile	Tyr	Lys	Asp	His	Ile	Thr	Leu	Met	Asp	Tyr	Glu	Ile	His	Glu
	50					55					60				

Gly	Phe	Asn	Phe	Glu	Leu	Tyr	Tyr	Gln
65					70			

&lt;210&gt; 23

&lt;211&gt; 66

&lt;212&gt; PRT

&lt;213&gt; Fasciola hepatica

&lt;400&gt; 23

Asp	Arg	Leu	Gly	Lys	Lys	Val	Arg	Val	Lys	Cys	Asn	Pro	Thr	Asp	Lys
1				5					10					15	

Val	Gly	Asp	Leu	Lys	Lys	Leu	Ile	Ala	Ala	Gln	Thr	Gly	Thr	Ala	Pro
			20					25					30		

Glu	Arg	Ile	Val	Leu	Lys	Lys	Trp	Tyr	Thr	Ile	Tyr	Lys	Asp	His	Val
		35					40					45			

Thr	Leu	Arg	Asp	Tyr	Glu	Ile	Asn	Asp	Gly	Met	Asn	Leu	Glu	Leu	Tyr
	50					55					60				

58

A



Tyr Gln  
65

<210> 24  
<211> 73  
<212> PRT  
<213> *Oryza sativa*

<400> 24  
Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Arg Val  
1 5 10 15  
Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala  
20 25 30  
Ala Gln Thr Gly Thr Arg Trp Asn Lys Ile Val Leu Lys Lys Trp Tyr  
35 40 45  
Thr Ile Tyr Lys Asp His Ile Thr Leu Ala Asp Tyr Glu Ile His Asp  
50 55 60  
Gly Met Gly Leu Glu Leu Tyr Tyr Asn  
65 70

<210> 25  
<211> 73  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 25  
Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Arg Val  
1 5 10 15  
Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala  
20 25 30  
Ala Gln Thr Gly Thr Arg Trp Asn Lys Ile Val Leu Lys Lys Trp Tyr  
35 40 45  
Thr Ile Leu Lys Asp His Ile Cys Leu Glu Asp Tyr Glu Val His Asp  
50 55 60  
Gln Thr Asn Leu Glu Leu Tyr Tyr Leu  
65 70

<210> 26  
<211> 76  
<212> PRT  
<213> *Homo sapiens*

<400> 26  
Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu  
1 5 10 15

59

A

Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp  
 20 25 30

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
 35 40 45

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu  
 50 55 60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly  
 65 70 75

<210> 27

<211> 60

<212> PRT

<213> Arabidopsis thaliana

<400> 27

Gly Lys Thr Ile Ile Leu Glu Val Glu Ser Ser Asp Thr Ile Ala Asn  
 1 5 10 15

Val Lys Glu Lys Ile Gln Val Lys Glu Gly Ile Lys Pro Asp Gln Gln  
 20 25 30

Met Leu Ile Phe Phe Gly Gln Gln Leu Glu Asp Gly Val Thr Leu Gly  
 35 40 45

Asp Tyr Asp Ile His Lys Lys Ser Thr Leu Tyr Leu  
 50 55 60

60

A